

SEQUENCE LISTING

<110> Roche Diagnostics GmbH

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thermostable DNA polymerases - for improvement of
nucleic acid synthesis and amplification in vitro

<130> 5304/OA/

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<170> PatentIn Ver. 2.1

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His Ile Val Ile Pro Trp Leu Lys Glu Asn Lys Pro Asp Ile Leu Cys	
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atg cag gag acg aag gtt gag aac agg aag ttt cct gag gcc gat ttt	144
Met Gln Glu Thr Lys Val Glu Asn Arg Lys Phe Pro Glu Ala Asp Phe	
35 40 45	
cac cgc atc ggc tac cac gtc gtc ttc agc ggg agc aag gga agg aat	192
His Arg Ile Gly Tyr His Val Phe Ser Gly Ser Lys Gly Arg Asn	
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gga gtg gcc ata gct tcc ctc gaa gag cct gag gat gtc agc ttc ggt	240
Gly Val Ala Ile Ala Ser Leu Glu Glu Pro Glu Asp Val Ser Phe Gly	
65 70 75 80	
ctc gat tca gag ccg aag gac gag gac agg ctg ata agg gca aag ata	288
Leu Asp Ser Glu Pro Lys Asp Glu Asp Arg Leu Ile Arg Ala Lys Ile	
85 90 95	
gct ggc ata gac gtg att aac acc tac gtt cct cag gga ttc aaa att	336
Ala Gly Ile Asp Val Ile Asn Thr Tyr Val Pro Gln Gly Phe Lys Ile	
100 105 110	
gac agc gag aag tac cag tac aag ctc cag tgg ctt gag agg ctt tac	384
Asp Ser Glu Lys Tyr Gln Tyr Lys Leu Gln Trp Leu Glu Arg Leu Tyr	
115 120 125	
cat tac ctt caa aaa acc gtt gac ttc aga agc ttt gct gtt tgg tgt	432
His Tyr Leu Gln Lys Thr Val Asp Phe Arg Ser Phe Ala Val Trp Cys	
130 135 140	
gga gac atg aac gtt gct cct gag cca atc gac gtt cac tcc cca gac	480
Gly Asp Met Asn Val Ala Pro Glu Pro Ile Asp Val His Ser Pro Asp	
145 150 155 160	

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

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 Lys Leu Lys Asn His Val Cys Phe His Glu Asp Ala Arg Arg Ala Tyr
 165 170 175

aaa aaa ata ctc gaa ctc ggc ttt gtt gac gtg ctg aga aaa ata cat 576
 Lys Lys Ile Leu Glu Leu Gly Phe Val Asp Val Leu Arg Lys Ile His
 180 185 190

ccc aac gag aga att tac acc ttc tac gac tac agg gtt aag gga gcc 624
 Pro Asn Glu Arg Ile Tyr Thr Phe Tyr Asp Tyr Arg Val Lys Gly Ala
 195 200 205

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 Ile Glu Arg Gly Leu Gly Trp Arg Val Asp Ala Ile Leu Ala Thr Pro
 210 215 220

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 Pro Leu Ala Glu Arg Cys Val Asp Cys Tyr Ala Asp Ile Lys Pro Arg
 225 230 235 240

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 Val

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Met Gln Glu Thr Lys Val Glu Asn Arg Lys Phe Pro Glu Ala Asp Phe
 35 40 45

His Arg Ile Gly Tyr His Val Val Phe Ser Gly Ser Lys Gly Arg Asn
 50 55 60

Gly Val Ala Ile Ala Ser Leu Glu Glu Pro Glu Asp Val Ser Phe Gly
 65 70 75 80

Leu Asp Ser Glu Pro Lys Asp Glu Asp Arg Leu Ile Arg Ala Lys Ile
 85 90 95

Ala Gly Ile Asp Val Ile Asn Thr Tyr Val Pro Gln Gly Phe Lys Ile
 100 105 110

Asp Ser Glu Lys Tyr Gln Tyr Lys Leu Gln Trp Leu Glu Arg Leu Tyr
 115 120 125

T06560"00000000

His Tyr Leu Gln Lys Thr Val Asp Phe Arg Ser Phe Ala Val Trp Cys
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Gly Asp Met Asn Val Ala Pro Glu Pro Ile Asp Val His Ser Pro Asp
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165 170 175

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180 185 190

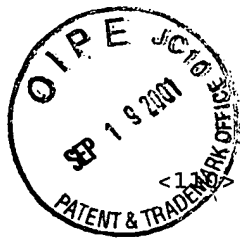
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210 215 220

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225 230 235 240

Leu Ala Glu Lys Pro Ser Asp His Leu Pro Leu Val Ala Val Phe Asp
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Val



SEQUENCE LISTING

ANKENBAUER, WALTRAUD

LAUE, FRANK

SOBEK, HERALD

GREIF, MICHAEL

<120> Thermostable Enzyme Promoting The Fidelity Of Thermostable DNA
 Polymerases -- For Improvement Of Nucleic Acid Synthesis And Amplification
 In Vitro

<130> 5304

<140> US 09/856,850

<141> 2001-05-25

<150> PCT/EP00/09423

<151> 2000-09-27

<150> EP/99119268.3

<151> 1999-09-28

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<170> PatentIn version 3.1

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His	Ile	Val	Ile	Pro	Trp	Leu	Lys	Glu	Asn	Lys	Pro	Asp	Ile	Leu	Cys	
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Gly	Val	Ala	Ile	Ala	Ser	Leu	Glu	Glu	Pro	Glu	Asp	Val	Ser	Phe	Gly	
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Leu	Asp	Ser	Glu	Pro	Lys	Asp	Glu	Asp	Arg	Leu	Ile	Arg	Ala	Lys	Ile	
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Ala	Gly	Ile	Asp	Val	Ile	Asn	Thr	Tyr	Val	Pro	Gln	Gly	Phe	Lys	Ile	
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gac	agc	gag	aag	tac	cag	tac	aag	ctc	cag	tgg	ctt	gag	agg	ctt	tac	384
Asp	Ser	Glu	Lys	Tyr	Gln	Tyr	Lys	Leu	Gln	Trp	Leu	Glu	Arg	Leu	Tyr	
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Gly	Asp	Met	Asn	Val	Ala	Pro	Glu	Pro	Ile	Asp	Val	His	Ser	Pro	Asp	
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Lys	Leu	Lys	Asn	His	Val	Cys	Phe	His	Glu	Asp	Ala	Arg	Arg	Ala	Tyr	
			165					170						175		
aaa	aaa	ata	ctc	gaa	ctc	ggc	ttt	gtt	gac	gtg	ctg	aga	aaa	ata	cat	576
Lys	Lys	Ile	Leu	Glu	Leu	Gly	Phe	Val	Asp	Val	Leu	Arg	Lys	Ile	His	
			180				185						190			
ccc	aac	gag	aga	att	tac	acc	ttc	tac	gac	tac	agg	gtt	aag	gga	gcc	624
Pro	Asn	Glu	Arg	Ile	Tyr	Thr	Phe	Tyr	Asp	Tyr	Arg	Val	Lys	Gly	Ala	
		195					200					205				
att	gag	cgg	ggg	ctg	gga	tgg	agg	gtt	gat	gcc	atc	ctc	gcc	acc	cca	672
Ile	Glu	Arg	Gly	Leu	Gly	Trp	Arg	Val	Asp	Ala	Ile	Leu	Ala	Thr	Pro	
	210					215					220					
ccc	ctc	gcc	gaa	aga	tgc	gtg	gac	tgc	tac	gca	gac	atc	aaa	ccg	agg	720
Pro	Leu	Ala	Glu	Arg	Cys	Val	Asp	Cys	Tyr	Ala	Asp	Ile	Lys	Pro	Arg	

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Leu Ala Glu Lys Pro Ser Asp His Leu Pro Leu Val Ala Val Phe Asp				
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gtg tag				774
Val				

<210> 18

<211> 257

<212> PRT

<213> Archaeoglobus fulgidus

<400> 18

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		20						25					30		

Met	Gln	Glu	Thr	Lys	Val	Glu	Asn	Arg	Lys	Phe	Pro	Glu	Ala	Asp	Phe
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His	Arg	Ile	Gly	Tyr	His	Val	Val	Phe	Ser	Gly	Ser	Lys	Gly	Arg	Asn
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Gly	Val	Ala	Ile	Ala	Ser	Leu	Glu	Glu	Pro	Glu	Asp	Val	Ser	Phe	Gly
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Leu	Asp	Ser	Glu	Pro	Lys	Asp	Glu	Asp	Arg	Leu	Ile	Arg	Ala	Lys	Ile
			85						90					95	

Ala	Gly	Ile	Asp	Val	Ile	Asn	Thr	Tyr	Val	Pro	Gln	Gly	Phe	Lys	Ile
			100					105					110		

Asp	Ser	Glu	Lys	Tyr	Gln	Tyr	Lys	Leu	Gln	Trp	Leu	Glu	Arg	Leu	Tyr
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His	Tyr	Leu	Gln	Lys	Thr	Val	Asp	Phe	Arg	Ser	Phe	Ala	Val	Trp	Cys
130						135					140				

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145 150 155 160

Lys Leu Lys Asn His Val Cys Phe His Glu Asp Ala Arg Arg Ala Tyr
165 170 175

Lys Lys Ile Leu Glu Leu Gly Phe Val Asp Val Leu Arg Lys Ile His
180 185 190

Pro Asn Glu Arg Ile Tyr Thr Phe Tyr Asp Tyr Arg Val Lys Gly Ala
195 200 205

Ile Glu Arg Gly Leu Gly Trp Arg Val Asp Ala Ile Leu Ala Thr Pro
210 215 220

Pro Leu Ala Glu Arg Cys Val Asp Cys Tyr Ala Asp Ile Lys Pro Arg
225 230 235 240

Leu Ala Glu Lys Pro Ser Asp His Leu Pro Leu Val Ala Val Phe Asp
245 250 255

Val